



OICE

RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/10/008,574A

TIME: 15:13:42

Input Set : A:\LEX-0264-USA SEQLIST.txt

Output Set: N:\CRF3\04082002\J008574A.raw

ENTERED

4 <110> APPLICANT: Walke, D. Wade
 5 Scoville, John
 7 <120> TITLE OF INVENTION: Novel Human 7TM Proteins and Polynucleotides Encoding the
 Same

9 <130> FILE REFERENCE: LEX-0264-USA

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/008,574A

C--> 11 <141> CURRENT FILING DATE: 2001-10-26

11 <150> PRIOR APPLICATION NUMBER: US 60/243,948

12 <151> PRIOR FILING DATE: 2000-10-27

14 <150> PRIOR APPLICATION NUMBER: US 60/244,291

15 <151> PRIOR FILING DATE: 2000-10-30

17 <160> NUMBER OF SEQ ID NOS: 5

19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 1923

23 <212> TYPE: DNA

24 <213> ORGANISM: homo sapiens

26 <400> SEQUENCE: 1

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29 tgcgatggtg tctgtacaga ctacccccag tgtactcaac cttgccctcc agacactcag      180
30 ggaaatatgg ggttttcatg caggcaaaag acatggcaca agatcactga cacctgccag      240
31 actcttaatg ccctcaacat ctttgaggag gattcacgtt tgggttcagcc atttgaagac      300
32 aatataaaaa taagtgtata tactggaaag tctgagacca taacagatat gttgctacaa      360
33 aagtgtccca cagatctgtc ttgtgtaatt agaaacattc agcagttctc ctggatacca      420
34 ggaaacattg ccgtaattgt gcagctctta cacaacatat caacagcaat atggacaggt      480
35 gttgatgagg caaagatgca gagttacagc accatagcca accacattct taacagcaaa      540
36 agcatctcca actggacttt cattcctgac agaaacagca gctatatact gctacattca      600
37 gtcaactcct ttgcaagaag gctattcata gataaacatc ctggtgacat atcagatgtc      660
38 ttcattcata ctatgggcac caccatatct ggagataaca ttggaaaaaa ttacactttt      720
39 tctatgagaa ttaatgatac cagcaatgaa gtcactggga gagtgttgat cagcagagat      780
40 gaacttcgga aggtgccttc ccttctcag gtcacagca ttgcatttcc aactattggg      840
41 gctatttttg aagccagtct tttggaaaat gttactgtaa atgggcttgt cctgtctgcc      900
42 attttgccca aggaacttaa aagaatctca ctgatttttg aaaagatcag caagtcagag      960
43 gagaggagga cacagtgtgt tggctggcac tctgtggaga acagatggga ccagcaggcc      1020
44 tgcaaaatga ttcaagaaaa ctcccagcaa gctgtttgca aatgtaggcc aagtgaattg      1080
45 ttacactctt tctcaattct tatgtcacct cacatcttag agagtctgat tctgacttac      1140
46 atcacatatg taggcctggg catttctatt tgcagcctga tcccttgctt gtccattgag      1200
47 gtcctagtct ggagccaagt gacaaagaca gagatcacct atttacgcca tgtgtgcatt      1260

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12 aaatgacatt tggccatttg tggcatcaat attgctgaca atgaactctg aaagagctat      1266

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53 ctacgacctg agatctgctg gctcaactgg gacatgacca aagccctcct ggccttcgtg      1620
54 atoccagctt tggccatcgt ggtagtaaac ctgatcacag tcacactggt gattgtcaag      1680
55 acccagcgag ctgccattgg caattccatg ttccaggaag tgagagccat tgtgagaatc      1740
56 agcaagaaca tcgccatcct cacaccactt ctgggactga cctgggggatt tggagtagcc      1800
57 actgtcatcg atgacagatc cctggccttc cacattatct tctccctgct caatgcattc      1860
58 caggtaagtc cagatgcttc tgaccaagtg caaagtgaga gaattcatga agatgttctg      1920
59 tga                                                                    1923
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62 <211> LENGTH: 640
63 <212> TYPE: PRT
64 <213> ORGANISM: homo sapiens
66 <400> SEQUENCE: 2
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68 1 5 10 15
69 Glu Ser Cys Arg Thr Leu Tyr Gln Ala Ala Ser Lys Ser Lys Glu Lys
70 20 25 30
71 Val Pro Ala Arg Pro His Gly Val Cys Asp Gly Val Cys Thr Asp Tyr
72 35 40 45
73 Pro Gln Cys Thr Gln Pro Cys Pro Pro Asp Thr Gln Gly Asn Met Gly
74 50 55 60
75 Phe Ser Cys Arg Gln Lys Thr Trp His Lys Ile Thr Asp Thr Cys Gln
76 65 70 75 80
77 Thr Leu Asn Ala Leu Asn Ile Phe Glu Glu Asp Ser Arg Leu Val Gln
78 85 90 95
79 Pro Phe Glu Asp Asn Ile Lys Ile Ser Val Tyr Thr Gly Lys Ser Glu
80 100 105 110
81 Thr Ile Thr Asp Met Leu Leu Gln Lys Cys Pro Thr Asp Leu Ser Cys
82 115 120 125
83 Val Ile Arg Asn Ile Gln Gln Ser Pro Trp Ile Pro Gly Asn Ile Ala
84 130 135 140
85 Val Ile Val Gln Leu Leu His Asn Ile Ser Thr Ala Ile Trp Thr Gly
86 145 150 155 160
87 Val Asp Glu Ala Lys Met Gln Ser Tyr Ser Thr Ile Ala Asn His Ile
88 165 170 175
89 Leu Asn Ser Lys Ser Ile Ser Asn Trp Thr Phe Ile Pro Asp Arg Asn
90 180 185 190
91 Ser Ser Tyr Ile Leu Leu His Ser Val Asn Ser Phe Ala Arg Arg Leu
92 195 200 205
93 Phe Ile Asp Lys His Pro Val Asp Ile Ser Asp Val Phe Ile His Thr
94 210 215 220
95 Met Gly Thr Thr Ile Ser Gly Asp Asn Ile Gly Lys Asn Phe Thr Phe
96 225 230 235 240
97 Ser Met Arg Ile Asn Asp Thr Ser Asn Glu Val Thr Gly Arg Val Leu
98 245 250 255
99 Ile Ser Arg Asp Glu Leu Arg Lys Val Pro Ser Pro Ser Gln Val Ile
100 260 265 270
101 Ser Ile Ala Phe Pro Thr Ile Gly Ala Ile Leu Glu Ala Ser Leu Leu
102 275 280 285
103 Glu Asn Val Thr Val Asn Glu Leu Val Ile Ser Ala Ile Thr Phe Leu

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105 Glu Leu Lys Arg Ile Ser Leu Ile Phe Glu Lys Ile Ser Lys Ser Glu
106 305      310      315      320
107 Glu Arg Arg Thr Gln Cys Val Gly Trp His Ser Val Glu Asn Arg Trp
108      325      330      335
109 Asp Gln Gln Ala Cys Lys Met Ile Gln Glu Asn Ser Gln Gln Ala Val
110      340      345      350
111 Cys Lys Cys Arg Pro Ser Glu Leu Phe Thr Ser Phe Ser Ile Leu Met
112      355      360      365
113 Ser Pro His Ile Leu Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr Val
114      370      375      380
115 Gly Leu Gly Ile Ser Ile Cys Ser Leu Ile Leu Cys Leu Ser Ile Glu
116 385      390      395      400
117 Val Leu Val Trp Ser Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu Arg
118      405      410      415
119 His Val Cys Ile Val Asn Ile Ala Ala Thr Leu Leu Met Ala Asp Val
120      420      425      430
121 Trp Phe Ile Val Ala Ser Phe Leu Ser Gly Pro Ile Thr His His Lys
122      435      440      445
123 Gly Cys Val Ala Ala Thr Phe Phe Val His Phe Phe Tyr Leu Ser Val
124      450      455      460
125 Phe Phe Trp Met Leu Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile Met
126 465      470      475      480
127 Ile Val Phe His Thr Leu Pro Lys Ser Val Leu Val Ala Ser Leu Phe
128      485      490      495
129 Ser Val Gly Tyr Gly Cys Pro Leu Ala Ile Ala Ala Ile Thr Val Ala
130      500      505      510
131 Ala Thr Glu Pro Gly Lys Gly Tyr Leu Arg Pro Glu Ile Cys Trp Leu
132      515      520      525
133 Asn Trp Asp Met Thr Lys Ala Leu Leu Ala Phe Val Ile Pro Ala Leu
134      530      535      540
135 Ala Ile Val Val Val Asn Leu Ile Thr Val Thr Leu Val Ile Val Lys
136 545      550      555      560
137 Thr Gln Arg Ala Ala Ile Gly Asn Ser Met Phe Gln Glu Val Arg Ala
138      565      570      575
139 Ile Val Arg Ile Ser Lys Asn Ile Ala Ile Leu Thr Pro Leu Leu Gly
140      580      585      590
141 Leu Thr Trp Gly Phe Gly Val Ala Thr Val Ile Asp Asp Arg Ser Leu
142      595      600      605
143 Ala Phe His Ile Ile Phe Ser Leu Leu Asn Ala Phe Gln Val Ser Pro
144      610      615      620
145 Asp Ala Ser Asp Gln Val Gln Ser Glu Arg Ile His Glu Asp Val Leu
146 625      630      635      640
148 <210> SEQ ID NO: 3
149 <211> LENGTH: 1737
150 <212> TYPE: DNA
151 <213> ORGANISM: homo sapiens
153 <400> SEQUENCE: 3
154 atgagagtttt catgcaggca aaagacatgg cagagagatga ctgag agttt aggttt tt

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155 aatgccctca acatctttga ggaggattca cgtttggttc agccatttga agacaatata 120
156 aaaataagtg tatatactgg aaagtctgag accataacag atatgttgct acaaaagtg 180
157 cccacagatc tgtcttggtg aattagaaac attcagcagt ctccctggat accaggaaac 240
158 attgccgtaa ttgtgcagct cttacacaac atatcaacag caatatggac aggtgttgat 300
159 gaggcaaaga tgcagagtta cagcaccata gccaacca tctttaacag caaaagcatc 360
160 tccaactgga ctttcattcc tgacagaaac agcagctata tctgtctaca ttcagtcaac 420
161 tcctttgcaa gaaggctatt catagataaa catcctgttg acatatcaga tgtcttcatt 480
162 catactatgg gcaccaccat atctggagat aacattggaa aaaatttcac tttttctatg 540
163 agaattaatg ataccagcaa tgaagtcact gggagagtgt tgatcagcag agatgaactt 600
164 cggaaggtgc cttccccttc tcaggtcac agcattgcat ttccaactat tggggctatt 660
165 ttggaagcca gtcttttggg aaatgttact gtaaattggg ttgtcctgtc tgccattttg 720
166 cccaaggaac ttaaaagaat ctactgatt ttgaaaaga tcagcaagtc agaggagagg 780
167 aggacacagt gtgttggtg gcactctgtg gagaacagat gggaccagca ggctgcaaa 840
168 atgattcaag aaaactccca gcaagctgtt tgcaaatgta ggccaagtga attgtttacc 900
169 tctttctcaa ttcttatgtc acctcacatc ttagagagtc tgattctgac ttacatcaca 960
170 tatgtaggcc tgggcatttc tatttgacgc ctgatccttt gcttgtccat tgaggctcta 1020
171 gtctggagcc aagtgacaaa gacagagatc acctatttac gccatgtgtg cattgttaac 1080
172 attgcagcca ctttgcctgt ggcagatgtg tggttcattg tggttcctt tcttagtggc 1140
173 ccaataacac accacaaggg atgtgtggca gccacatttt ttgttcattt cttttacctt 1200
174 tctgtatttt tctggatgct tgccaaggca ctccctatcc tctatggaat catgattgtt 1260
175 ttccatacct tgcccaagtc agtctgtgtg gcactctctg tttcagtggg ctatggatgc 1320
176 cctttggcca ttgctgccat cactgttgc gccactgaac ctggcaaagg ctatctacga 1380
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178 gctttggcca tctgtgtagt aaacctgac acagtccac tggtgattgt caagaccag 1500
179 cgagctgcca ttggcaattc catgttcag gaagtgcag ccattgtgag aatcagcaag 1560
180 aacatgcgca tcttcacacc acttctggga ctgacctggg gatttggagt agccactgtc 1620
181 atcgatgaca gatccctggc cttccacatt atcttctccc tgetcaatgc attccaggta 1680
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184 <210> SEQ ID NO: 4

185 <211> LENGTH: 578

186 <212> TYPE: PRT

187 <213> ORGANISM: homo sapiens

189 <400> SEQUENCE: 4

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192 Cys Gln Thr Leu Asn Ala Leu Asn Ile Phe Glu Glu Asp Ser Arg Leu
193 20 25 30
194 Val Gln Pro Phe Glu Asp Asn Ile Lys Ile Ser Val Tyr Thr Gly Lys
195 35 40 45
196 Ser Glu Thr Ile Thr Asp Met Leu Leu Gln Lys Cys Pro Thr Asp Leu
197 50 55 60
198 Ser Cys Val Ile Arg Asn Ile Gln Gln Ser Pro Trp Ile Pro Gly Asn
199 65 70 75 80
200 Ile Ala Val Ile Val Gln Leu Leu His Asn Ile Ser Thr Ala Ile Trp
201 85 90 95
202 Thr Gly Val Asp Glu Ala Lys Met Gln Ser Tyr Ser Thr Ile Ala Asn
203 100 105 110
204 His Ile Leu Asn Ser Lys Ser Ile Ser Asn Trp Thr Phe Ile Pro Asp
205 115 120 125

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206 Arg Asn Ser Ser Tyr Ile Leu Leu His Ser Val Asn Ser Phe Ala Arg
207      130      135      140
208 Arg Leu Phe Ile Asp Lys His Pro Val Asp Ile Ser Asp Val Phe Ile
209 145      150      155      160
210 His Thr Met Gly Thr Thr Ile Ser Gly Asp Asn Ile Gly Lys Asn Phe
211      165      170      175
212 Thr Phe Ser Met Arg Ile Asn Asp Thr Ser Asn Glu Val Thr Gly Arg
213      180      185      190
214 Val Leu Ile Ser Arg Asp Glu Leu Arg Lys Val Pro Ser Pro Ser Gln
215      195      200      205
216 Val Ile Ser Ile Ala Phe Pro Thr Ile Gly Ala Ile Leu Glu Ala Ser
217      210      215      220
218 Leu Leu Glu Asn Val Thr Val Asn Gly Leu Val Leu Ser Ala Ile Leu
219 225      230      235      240
220 Pro Lys Glu Leu Lys Arg Ile Ser Leu Ile Phe Glu Lys Ile Ser Lys
221      245      250      255
222 Ser Glu Glu Arg Arg Thr Gln Cys Val Gly Trp His Ser Val Glu Asn
223      260      265      270
224 Arg Trp Asp Gln Gln Ala Cys Lys Met Ile Gln Glu Asn Ser Gln Gln
225      275      280      285
226 Ala Val Cys Lys Cys Arg Pro Ser Glu Leu Phe Thr Ser Phe Ser Ile
227      290      295      300
228 Leu Met Ser Pro His Ile Leu Glu Ser Leu Ile Leu Thr Tyr Ile Thr
229 305      310      315      320
230 Tyr Val Gly Leu Gly Ile Ser Ile Cys Ser Leu Ile Leu Cys Leu Ser
231      325      330      335
232 Ile Glu Val Leu Val Trp Ser Gln Val Thr Lys Thr Glu Ile Thr Tyr
233      340      345      350
234 Leu Arg His Val Cys Ile Val Asn Ile Ala Ala Thr Leu Leu Met Ala
235      355      360      365
236 Asp Val Trp Phe Ile Val Ala Ser Phe Leu Ser Gly Pro Ile Thr His
237      370      375      380
238 His Lys Gly Cys Val Ala Ala Thr Phe Phe Val His Phe Phe Tyr Leu
239 385      390      395      400
240 Ser Val Phe Phe Trp Met Leu Ala Lys Ala Leu Leu Ile Leu Tyr Gly
241      405      410      415
242 Ile Met Ile Val Phe His Thr Leu Pro Lys Ser Val Leu Val Ala Ser
243      420      425      430
244 Leu Phe Ser Val Gly Tyr Gly Cys Pro Leu Ala Ile Ala Ala Ile Thr
245      435      440      445
246 Val Ala Ala Thr Glu Pro Gly Lys Gly Tyr Leu Arg Pro Glu Ile Cys
247      450      455      460
248 Trp Leu Asn Trp Asp Met Thr Lys Ala Leu Leu Ala Phe Val Ile Pro
249 465      470      475      480
250 Ala Leu Ala Ile Val Val Val Asn Leu Ile Thr Val Thr Leu Val Ile
251      485      490      495
252 Val Lys Thr Gln Arg Ala Ala Ile Gly Asn Ser Met Phe Gln Glu Val
253      500      505      510
254 Arg Ala Ile Val Arg Ile Ser Lys Asp Ile Ala Ile Leu Thr Phe Ile

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VERIFICATION SUMMARY

DATE: 04/08/2002

PATENT APPLICATION: US/10/008,574A

TIME: 15:13:43

Input Set : A:\LEX-0264-USA SEQLIST.txt

Output Set: N:\CRF3\04082002\J008574A.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date